SEQUENCE LISTING

<110> Ni, Jian
Yu, Guo-Liang
Fan, Ping
Gentz, Reiner L.

<120> Human Tumor Necrosis Factor Receptor TR9

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agaagcagcc gccgattcca gctgccccgc gcgccccggg cgcccctgcg agtccccggt 240

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       Met Gly Thr Ser Pro Ser Ser Ser Thr Ala Leu Ala Ser Cys
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agc cgc atc gcc cgc cga gcc aca gcc acg atg atc gcg ggc tcc ctt   336
Ser Arg Ile Ala Arg Arg Ala Thr Ala Thr Met Ile Ala Gly Ser Leu
    -25                 -20                 -15

ctc ctg ctt gga ttc ctt agc acc acc aca gct cag cca gaa cag aag   384
Leu Leu Leu Gly Phe Leu Ser Thr Thr Thr Ala Gln Pro Glu Gln Lys
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gcc tcg aat ctc att ggc aca tac cgc cat gtt gac cgt gcc acc ggc   432
Ala Ser Asn Leu Ile Gly Thr Tyr Arg His Val Asp Arg Ala Thr Gly
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cag gtg cta acc tgt gac aag tgt cca gca gga acc tat gtc tct gag   480
Gln Val Leu Thr Cys Asp Lys Cys Pro Ala Gly Thr Tyr Val Ser Glu
        25                  30                  35

cat tgt acc aac aca agc ctg cgc gtc tgc agc agt tgc cct gtg ggg   528
His Cys Thr Asn Thr Ser Leu Arg Val Cys Ser Ser Cys Pro Val Gly
    40                  45                  50

acc ttt acc agg cat gag aat ggc ata gag aaa tgc cat gac tgt agt   576
Thr Phe Thr Arg His Glu Asn Gly Ile Glu Lys Cys His Asp Cys Ser
55                  60                  65                  70

cag cca tgc cca tgg cca atg att gag aaa tta cct tgt gct gcc ttg   624
Gln Pro Cys Pro Trp Pro Met Ile Glu Lys Leu Pro Cys Ala Ala Leu
                75                  80                  85

act gac cga gaa tgc act tgc cca cct ggc atg ttc cag tct aac gct   672
Thr Asp Arg Glu Cys Thr Cys Pro Pro Gly Met Phe Gln Ser Asn Ala
            90                  95                  100

acc tgt gcc ccc cat acg gtg tgt cct gtg ggt tgg ggt gtg cgg aag   720
Thr Cys Ala Pro His Thr Val Cys Pro Val Gly Trp Gly Val Arg Lys
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aaa ggg aca gag act gag gat gtg cgg tgt aag cag tgt gct cgg ggt   768
Lys Gly Thr Glu Thr Glu Asp Val Arg Cys Lys Gln Cys Ala Arg Gly
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acc ttc tca gat gtg cct tct agt gtg atg aaa tgc aaa gca tac aca   816
Thr Phe Ser Asp Val Pro Ser Ser Val Met Lys Cys Lys Ala Tyr Thr
135                 140                 145                 150

gac tgt ctg agt cag aac ctg gtg gtg atc aag ccg ggg acc aag gag   864
Asp Cys Leu Ser Gln Asn Leu Val Val Ile Lys Pro Gly Thr Lys Glu
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aca gac aac gtc tgt ggc aca ctc ccg tcc ttc tcc agc tcc acc tca   912
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cct tcc cct ggc aca gcc atc ttt cca cgc cct gag cac atg gaa acc   960
Pro Ser Pro Gly Thr Ala Ile Phe Pro Arg Pro Glu His Met Glu Thr
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cat gaa gtc cct tcc tcc act tat gtt ccc aaa ggc atg aac tca aca   1008
His Glu Val Pro Ser Ser Thr Tyr Val Pro Lys Gly Met Asn Ser Thr
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gaa tcc aac tct tct gcc tct gtt aga cca aag gta ctg agt agc atc   1056
Glu Ser Asn Ser Ser Ala Ser Val Arg Pro Lys Val Leu Ser Ser Ile
215                 220                 225                 230

cag gaa ggg aca gtc cct gac aac aca agc tca gca agg ggg aag gaa   1104
Gln Glu Gly Thr Val Pro Asp Asn Thr Ser Ser Ala Arg Gly Lys Glu
                235                 240                 245

gac gtg aac aag acc ctc cca aac ctt cag gta gtc aac cac cag caa   1152
Asp Val Asn Lys Thr Leu Pro Asn Leu Gln Val Val Asn His Gln Gln
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ggc ccc cac cac aga cac atc ctg aag ctg ctg ccg tcc atg gag gcc   1200
Gly Pro His His Arg His Ile Leu Lys Leu Leu Pro Ser Met Glu Ala
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act ggg ggc gag aag tcc agc acg ccc atc aag ggc ccc aag agg gga   1248
Thr Gly Gly Glu Lys Ser Ser Thr Pro Ile Lys Gly Pro Lys Arg Gly
    280                 285                 290

cat cct aga cag aac cta cac aag cat ttt gac atc aat gag cat ttg   1296
His Pro Arg Gln Asn Leu His Lys His Phe Asp Ile Asn Glu His Leu
295                 300                 305                 310

ccc tgg atg att gtg ctt ttc ctg ctg ctg gtg ctt gtg gtg att gtg   1344
Pro Trp Met Ile Val Leu Phe Leu Leu Leu Val Leu Val Val Ile Val
                315                 320                 325

gtg tgc agt atc cgg aaa agc tcg agg act ctg aaa aag ggg ccc cgg   1392
Val Cys Ser Ile Arg Lys Ser Ser Arg Thr Leu Lys Lys Gly Pro Arg
            330                 335                 340

cag gat ccc agt gcc att gtg gaa aag gca ggg ctg aag aaa tcc atg   1440
Gln Asp Pro Ser Ala Ile Val Glu Lys Ala Gly Leu Lys Lys Ser Met
        345                 350                 355

act cca acc cag aac cgg gag aaa tgg atc tac tac tgc aat ggc cat   1488
Thr Pro Thr Gln Asn Arg Glu Lys Trp Ile Tyr Tyr Cys Asn Gly His
    360                 365                 370

ggt atc gat atc ctg aag ctt gta gca gcc caa gtg gga agc cag tgg   1536
Gly Ile Asp Ile Leu Lys Leu Val Ala Ala Gln Val Gly Ser Gln Trp
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aaa gat atc tat cag ttt ctt tgc aat gcc agt gag agg gag gtt gct   1584
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gct ttc tcc aat ggg tac aca gcc gac cac gag cgg gcc tac gca gct      1632
Ala Phe Ser Asn Gly Tyr Thr Ala Asp His Glu Arg Ala Tyr Ala Ala
            410                 415                 420

ctg cag cac tgg acc atc cgg ggc ccc gag gcc agc ctc gcc cag cta      1680
Leu Gln His Trp Thr Ile Arg Gly Pro Glu Ala Ser Leu Ala Gln Leu
        425                 430                 435

att agc gcc ctg cgc cag cac cgg aga aac gat gtt gtg gag aag att      1728
Ile Ser Ala Leu Arg Gln His Arg Arg Asn Asp Val Val Glu Lys Ile
    440                 445                 450

cgt ggg ctg atg gaa gac acc acc cag ctg gaa act gac aaa cta gct      1776
Arg Gly Leu Met Glu Asp Thr Thr Gln Leu Glu Thr Asp Lys Leu Ala
455                 460                 465                 470

ctc ccg atg agc ccc agc ccg ctt agc ccg agc ccc atc ccc agc ccc      1824
Leu Pro Met Ser Pro Ser Pro Leu Ser Pro Ser Pro Ile Pro Ser Pro
                475                 480                 485

aac gcg aaa ctt gag aat tcc gct ctc ctg acg gtg gag cct tcc cca      1872
Asn Ala Lys Leu Glu Asn Ser Ala Leu Leu Thr Val Glu Pro Ser Pro
            490                 495                 500

cag gac aag aac aag ggc ttc ttc gtg gat gag tcg gag ccc ctt ctc      1920
Gln Asp Lys Asn Lys Gly Phe Phe Val Asp Glu Ser Glu Pro Leu Leu
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cgc tgt gac tct aca tcc agc ggc tcc tcc gcg ctg agc agg aac ggt      1968
Arg Cys Asp Ser Thr Ser Ser Gly Ser Ser Ala Leu Ser Arg Asn Gly
    520                 525                 530

tcc ttt att acc aaa gaa aag aag gac aca gtg ttg cgg cag gta cgc      2016
Ser Phe Ile Thr Lys Glu Lys Lys Asp Thr Val Leu Arg Gln Val Arg
535                 540                 545                 550

ctg gac ccc tgt gac ttg cag cct atc ttt gat gac atg ctc cac ttt      2064
Leu Asp Pro Cys Asp Leu Gln Pro Ile Phe Asp Asp Met Leu His Phe
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cta aat cct gag gag ctg cgg gtg att gaa gag att ccc cag gct gag      2112
Leu Asn Pro Glu Glu Leu Arg Val Ile Glu Glu Ile Pro Gln Ala Glu
            570                 575                 580

gac aaa cta gac cgg cta ttc gaa att att gga gtc aag agc cag gaa      2160
Asp Lys Leu Asp Arg Leu Phe Glu Ile Ile Gly Val Lys Ser Gln Glu
        585                 590                 595

gcc agc cag acc ctc ctg gac tct gtt tat agc cat ctt cct gac ctg      2208
Ala Ser Gln Thr Leu Leu Asp Ser Val Tyr Ser His Leu Pro Asp Leu
    600                 605                 610
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ctg tagaacatag ggatactgca ttctggaaat tactcaattt agtggcaggg 2261
Leu
615

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atacacataa tcaataggtc caatctgctc tcaaggcctt ggtcctggtg ggattccttc 3221

accaattact ttaattaaaa atggctgcaa ctgtaagaac ccttgtctga tatatttgca 3281

actatgctcc catttacaaa tgtaccttct aatgctcagt tgccaggttc caatgcaaag 3341

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Asn Leu Ile Gly Thr Tyr Arg His Val Asp Arg Ala Thr Gly Gln Val
     10                  15                  20

Leu Thr Cys Asp Lys Cys Pro Ala Gly Thr Tyr Val Ser Glu His Cys
 25                  30                  35                  40

Thr Asn Thr Ser Leu Arg Val Cys Ser Ser Cys Pro Val Gly Thr Phe
                45                  50                  55

Thr Arg His Glu Asn Gly Ile Glu Lys Cys His Asp Cys Ser Gln Pro
            60                  65                  70

Cys Pro Trp Pro Met Ile Glu Lys Leu Pro Cys Ala Ala Leu Thr Asp
        75                  80                  85

Arg Glu Cys Thr Cys Pro Pro Gly Met Phe Gln Ser Asn Ala Thr Cys
     90                  95                  100

Ala Pro His Thr Val Cys Pro Val Gly Trp Gly Val Arg Lys Lys Gly
105                 110                 115                 120

Thr Glu Thr Glu Asp Val Arg Cys Lys Gln Cys Ala Arg Gly Thr Phe
                125                 130                 135

Ser Asp Val Pro Ser Ser Val Met Lys Cys Lys Ala Tyr Thr Asp Cys
            140                 145                 150

Leu Ser Gln Asn Leu Val Val Ile Lys Pro Gly Thr Lys Glu Thr Asp
        155                 160                 165

Asn Val Cys Gly Thr Leu Pro Ser Phe Ser Ser Ser Thr Ser Pro Ser
    170                 175                 180

Pro Gly Thr Ala Ile Phe Pro Arg Pro Glu His Met Glu Thr His Glu
185                 190                 195                 200

Val Pro Ser Ser Thr Tyr Val Pro Lys Gly Met Asn Ser Thr Glu Ser
                205                 210                 215

Asn Ser Ser Ala Ser Val Arg Pro Lys Val Leu Ser Ser Ile Gln Glu
            220                 225                 230

Gly Thr Val Pro Asp Asn Thr Ser Ser Ala Arg Gly Lys Glu Asp Val
        235                 240                 245

Asn Lys Thr Leu Pro Asn Leu Gln Val Val Asn His Gln Gln Gly Pro
    250                 255                 260
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His His Arg His Ile Leu Lys Leu Leu Pro Ser Met Glu Ala Thr Gly
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Gly Glu Lys Ser Ser Thr Pro Ile Lys Gly Pro Lys Arg Gly His Pro
285 290 295

Arg Gln Asn Leu His Lys His Phe Asp Ile Asn Glu His Leu Pro Trp
300 305 310

Met Ile Val Leu Phe Leu Leu Leu Val Leu Val Val Ile Val Val Cys
315 320 325

Ser Ile Arg Lys Ser Ser Arg Thr Leu Lys Lys Gly Pro Arg Gln Asp
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Pro Ser Ala Ile Val Glu Lys Ala Gly Leu Lys Lys Ser Met Thr Pro
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Thr Gln Asn Arg Glu Lys Trp Ile Tyr Tyr Cys Asn Gly His Gly Ile
365 370 375

Asp Ile Leu Lys Leu Val Ala Ala Gln Val Gly Ser Gln Trp Lys Asp
380 385 390

Ile Tyr Gln Phe Leu Cys Asn Ala Ser Glu Arg Glu Val Ala Ala Phe
395 400 405

Ser Asn Gly Tyr Thr Ala Asp His Glu Arg Ala Tyr Ala Ala Leu Gln
410 415 420

His Trp Thr Ile Arg Gly Pro Glu Ala Ser Leu Ala Gln Leu Ile Ser
425 430 435 440

Ala Leu Arg Gln His Arg Arg Asn Asp Val Val Glu Lys Ile Arg Gly
445 450 455

Leu Met Glu Asp Thr Thr Gln Leu Glu Thr Asp Lys Leu Ala Leu Pro
460 465 470

Met Ser Pro Ser Pro Leu Ser Pro Ser Pro Ile Pro Ser Pro Asn Ala
475 480 485

Lys Leu Glu Asn Ser Ala Leu Leu Thr Val Glu Pro Ser Pro Gln Asp
490 495 500

Lys Asn Lys Gly Phe Phe Val Asp Glu Ser Glu Pro Leu Leu Arg Cys
505 510 515 520

Asp Ser Thr Ser Ser Gly Ser Ser Ala Leu Ser Arg Asn Gly Ser Phe
525 530 535

Ile Thr Lys Glu Lys Lys Asp Thr Val Leu Arg Gln Val Arg Leu Asp
540 545 550

Pro Cys Asp Leu Gln Pro Ile Phe Asp Asp Met Leu His Phe Leu Asn

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        555                 560                 565

Pro Glu Glu Leu Arg Val Ile Glu Glu Ile Pro Gln Ala Glu Asp Lys
    570                 575                 580

Leu Asp Arg Leu Phe Glu Ile Ile Gly Val Lys Ser Gln Glu Ala Ser
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Gln Thr Leu Leu Asp Ser Val Tyr Ser His Leu Pro Asp Leu Leu
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            20                  25                  30

Lys Gly Leu Glu Leu Arg Lys Thr Val Thr Thr Val Glu Thr Gln Asn
        35                  40                  45

Leu Glu Gly Leu His His Asp Gly Gln Phe Cys His Lys Pro Cys Pro
    50                  55                  60

Pro Gly Glu Arg Lys Ala Arg Asp Cys Thr Val Asn Gly Asp Glu Pro
65                  70                  75                  80

Asp Cys Val Pro Cys Gln Glu Gly Lys Glu Tyr Thr Asp Lys Ala His
                85                  90                  95

Phe Ser Ser Lys Cys Arg Arg Cys Arg Leu Cys Asp Glu Gly His Gly
            100                 105                 110

Leu Glu Val Glu Ile Asn Cys Thr Arg Thr Gln Asn Thr Lys Cys Arg
        115                 120                 125

Cys Lys Pro Asn Phe Phe Cys Asn Ser Thr Val Cys Glu His Cys Asp
    130                 135                 140

Pro Cys Thr Lys Cys Glu His Gly Ile Ile Lys Glu Cys Thr Leu Thr
145                 150                 155                 160

Ser Asn Thr Lys Cys Lys Glu Glu Gly Ser Arg Ser Asn Leu Gly Trp
                165                 170                 175

Leu Cys Leu Leu Leu Leu Pro Ile Pro Leu Ile Val Trp Val Lys Arg
            180                 185                 190
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Lys Glu Val Gln Lys Thr Cys Arg Lys His Arg Lys Glu Asn Gln Gly
195 200 205

Ser His Glu Ser Pro Thr Leu Asn Pro Glu Thr Val Ala Ile Asn Leu
210 215 220

Ser Asp Val Asp Leu Ser Lys Tyr Ile Thr Thr Ile Ala Gly Val Met
225 230 235 240

Thr Leu Ser Gln Val Lys Ala Asn Leu Cys Thr Leu Ala Glu Lys Ile
245 250 255

Gln Thr Ile Ile Leu Lys Asp Ile Thr Ser Asp Ser Glu Asn Ser Asn
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Phe Arg Asn Glu Ile Gln Ser Leu Val
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35 40 45

Leu Gly Glu Gly Val Ala Gln Pro Cys Gly Ala Asn Gln Thr Val Cys
50 55 60

Glu Pro Cys Leu Asp Ser Val Thr Phe Ser Asp Val Val Ser Ala Thr
65 70 75 80

Glu Pro Cys Lys Pro Cys Thr Glu Cys Val Gly Leu Gln Ser Met Ser
85 90 95

Ala Pro Cys Val Glu Ala Asp Asp Ala Val Cys Arg Cys Ala Tyr Gly
100 105 110

Tyr Tyr Gln Asp Glu Thr Thr Gly Arg Cys Glu Ala Cys Arg Val Cys
115 120 125

Glu Ala Gly Ser Gly Leu Val Phe Ser Cys Gln Asp Lys Gln Asn Thr
130 135 140

Val Cys Glu Glu Cys Pro Asp Gly Thr Tyr Ser Asp Glu Ala Asn His
145 150 155 160

Val Asp Pro Cys Leu Pro Cys Thr Val Cys Glu Asp Thr Glu Arg Gln
165 170 175

Leu Arg Glu Cys Thr Arg Trp Ala Asp Ala Glu Cys Glu Glu Ile Pro
180 185 190

Gly Arg Trp Ile Thr Arg Ser Thr Pro Pro Glu Gly Ser Asp Ser Thr
195 200 205

Ala Pro Ser Thr Gln Glu Pro Glu Ala Pro Pro Glu Gln Asp Leu Ile
210 215 220

Ala Ser Thr Val Ala Gly Val Val Thr Thr Val Met Gly Ser Ser Gln
225 230 235 240

Pro Val Val Thr Arg Gly Thr Thr Asp Asn Leu Ile Pro Val Tyr Cys
245 250 255

Ser Ile Leu Ala Ala Val Val Val Gly Leu Val Ala Tyr Ile Ala Phe
260 265 270

Lys Arg Trp Asn Ser Cys Lys Gln Asn Lys Gln Gly Ala Asn Ser Arg
275 280 285

Pro Val Asn Gln Thr Pro Pro Pro Glu Gly Glu Lys Leu His Ser Asp
290 295 300

Ser Gly Ile Ser Val Asp Ser Gln Ser Leu His Asp Gln Gln Pro His
305 310 315 320

Thr Gln Thr Ala Ser Gly Gln Ala Leu Lys Gly Asp Gly Gly Leu Tyr
325 330 335

Ser Ser Leu Pro Pro Ala Lys Arg Glu Glu Val Glu Lys Leu Leu Asn
340 345 350

Gly Ser Ala Gly Asp Thr Trp Arg His Leu Ala Gly Glu Leu Gly Tyr
355 360 365

Gln Pro Glu His Ile Asp Ser Phe Thr His Glu Ala Cys Pro Val Arg
370 375 380

Ala Leu Leu Ala Ser Trp Ala Thr Gln Asp Ser Ala Thr Leu Pro Arg
385 390 395 400

Arg Glu Val Ala Pro Pro Tyr Gln Gly Ala Asp Pro Ile Leu Ala Thr
405 410 415

Ala Leu Ala Ser Asp Pro Ile Pro Asn Pro Leu Gln Lys Trp Glu Asp
420 425 430

Ser Ala His Lys Pro Gln Ser Leu Asp Thr Asp Asp Pro Cys Ser Glu
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Ser Thr Ala Thr Ser Pro Val

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            20                  25                  30

His Leu Gly Asp Arg Glu Lys Arg Asp Ser Val Cys Pro Gln Gly Lys
        35                  40                  45

Tyr Ile His Pro Gln Asn Asn Ser Ile Cys Cys Thr Lys Cys His Lys
    50                  55                  60

Gly Thr Tyr Leu Tyr Asn Asp Cys Pro Gly Pro Gly Gln Asp Thr Asp
65                  70                  75                  80

Cys Arg Glu Cys Glu Ser Gly Ser Phe Thr Ala Ser Glu Asn His Leu
                85                  90                  95

Arg His Cys Leu Ser Cys Ser Lys Cys Arg Lys Glu Met Gly Gln Val
            100                 105                 110

Glu Ile Ser Ser Cys Thr Val Asp Arg Asp Thr Val Cys Gly Cys Arg
        115                 120                 125

Lys Asn Gln Tyr Arg His Tyr Trp Ser Glu Asn Leu Phe Gln Cys Phe
    130                 135                 140

Asn Cys Ser Leu Cys Leu Asn Gly Thr Val His Leu Ser Cys Gln Glu
145                 150                 155                 160

Lys Gln Asn Thr Val Cys Thr Cys His Ala Gly Phe Phe Leu Arg Glu
                165                 170                 175

Asn Glu Cys Val Ser Cys Ser Asn Cys Lys Lys Ser Leu Glu Cys Thr
            180                 185                 190

Lys Leu Cys Leu Pro Gln Ile Glu Asn Val Lys Gly Thr Glu Asp Ser
        195                 200                 205

Gly Thr Thr Val Leu Leu Pro Leu Val Ile Phe Phe Gly Leu Cys Leu
    210                 215                 220

Leu Ser Leu Leu Phe Ile Gly Leu Met Tyr Arg Tyr Gln Arg Trp Lys
225                 230                 235                 240

Ser Lys Leu Tyr Ser Ile Val Cys Gly Lys Ser Thr Pro Glu Lys Glu
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Gly Glu Leu Glu Gly Thr Thr Thr Lys Pro Leu Ala Pro Asn Pro Ser
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Phe Ser Pro Thr Pro Gly Phe Thr Pro Thr Leu Gly Phe Ser Pro Val
        275                 280                 285

Pro Ser Ser Thr Phe Thr Ser Ser Ser Thr Tyr Thr Pro Gly Asp Cys
    290                 295                 300

Pro Asn Phe Ala Ala Pro Arg Arg Glu Val Ala Pro Pro Tyr Gln Gly
305                 310                 315                 320

Ala Asp Pro Ile Leu Ala Thr Ala Leu Ala Ser Asp Pro Ile Pro Asn
                325                 330                 335

Pro Leu Gln Lys Trp Glu Asp Ser Ala His Lys Pro Gln Ser Leu Asp
            340                 345                 350

Thr Asp Asp Pro Ala Thr Leu Tyr Ala Val Val Glu Asn Val Pro Pro
        355                 360                 365

Leu Arg Trp Lys Glu Phe Val Arg Arg Leu Gly Leu Ser Asp His Glu
    370                 375                 380

Ile Asp Arg Leu Glu Leu Gln Asn Gly Arg Cys Leu Arg Glu Ala Gln
385                 390                 395                 400

Tyr Ser Met Leu Ala Thr Trp Arg Arg Arg Thr Pro Arg Arg Glu Ala
                405                 410                 415

Thr Leu Glu Leu Leu Gly Arg Val Leu Arg Asp Met Asp Leu Leu Gly
            420                 425                 430

Cys Leu Glu Asp Ile Glu Glu Ala Leu Cys Gly Pro Ala Ala Leu Pro
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Pro Ala Pro Ser Leu Leu Arg
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aacgcgaaac ttgagaattc cgctctcctg acggtggagc cttccccaca ggacaagaac 180
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agcccgagcc ccatccccag ccccaacgcg aaacttgaga attccgctct cctgacggtg 180
gagcctttcc cacaggacaa gaacaagggc ttcttcgtgg atgagtcgga gccccttctc 240
cgctgtactc tacatccagc ggctcctccg gctgagcagg aacggttcct ttattaccaa 300
gaaaagaagg acacag 316

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<213> Homo sapiens

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attaagaaaa tttaagaccc cattgagtta ctgtaatgca attcaacttt gagttatctt 180
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gtatggttca cctggcaccg tgtagatgct tgattacttg tactctctta tgtaaatgct 300
ctgggctggg gaatgaatcc caggctcagg tttccctatt aaggggttca ctggccccaa 360
gactgactcc cttggggttg ggtttggaca atgtcttggg agaaaagccg gggcttccag 420
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<211> 26
<212> DNA
<213> Homo sapiens

<400> 11
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<210> 12
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<212> DNA
<213> Homo sapiens

<400> 12
cgcaagcttt tagggcaaat gctcattg 28

<210> 13
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<400> 13
cgccccgggg ccatcatggg gacctctccg agc 33

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<211> 28
<212> DNA
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<400> 14
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<212> DNA
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.1> 31
l2> DNA
l3> Homo sapiens

)0> 17
atcttcct gacctgctgt agtctagagc c 31

10> 18
11> 30
12> DNA
13> Homo sapiens

00> 18
cgaccacg agcgggccta gtctagagcc 30

:10> 19
:11> 147
:12> PRT
:13> Homo sapiens

100> 19
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1 5 10 15

sn Thr Ser Leu Arg Val Cys Ser Ser Cys Pro Val Gly Thr Phe Thr
20 25 30

rg His Glu Asn Gly Ile Glu Lys Cys His Asp Cys Ser Gln Pro Cys
35 40 45

ro Trp Pro Met Ile Glu Lys Leu Pro Cys Ala Ala Leu Thr Asp Arg
50 55 60

lu Cys Thr Cys Pro Pro Gly Met Phe Gln Ser Asn Ala Thr Cys Ala
65 70 75 80

ro His Thr Val Cys Pro Val Gly Trp Gly Val Arg Lys Lys Gly Thr
85 90 95

lu Thr Glu Asp Val Arg Cys Lys Gln Cys Ala Arg Gly Thr Phe Ser
100 105 110

sp Val Pro Ser Ser Val Met Pro Cys Lys Ala Tyr Thr Asp Cys Leu
115 120 125

er Gln Asn Leu Val Val Ile Lys Pro Gly Thr Lys Glu Thr Asp Asn

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Val Cys Gly
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<210> 20
<211> 147
<212> PRT
<213> Homo sapiens

<400> 20

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             20                  25                  30

Asp Ser Trp His Thr Ser Asp Glu Cys Leu Tyr Cys Ser Pro Val Cys
         35                  40                  45

Lys Glu Leu Gln Tyr Val Lys Gln Glu Cys Asn Arg Thr His Asn Arg
     50                  55                  60

Val Cys Glu Cys Lys Glu Gly Arg Tyr Leu Glu Ile Glu Phe Cys Leu
 65                  70                  75                  80

Lys His Arg Ser Cys Pro Pro Gly Phe Gly Val Val Gln Ala Gly Thr
                 85                  90                  95

Pro Glu Arg Asn Thr Val Cys Lys Arg Cys Pro Asp Gly Phe Phe Ser
            100                 105                 110

Asn Glu Thr Ser Ser Lys Ala Pro Cys Arg Lys His Thr Asn Cys Ser
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Val Phe Gly Leu Leu Leu Thr Gln Lys Gly Asn Ala Thr His Asp Asn
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Ile Cys Ser
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<210> 21
<211> 67
<212> PRT
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<400> 21

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Val Ala Ala Phe Ser Asn Gly Tyr Thr Ala Asp His Glu Arg Ala Tyr
             20                  25                  30
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Ala Ala Leu Gln His Trp Thr Ile Arg Gly Pro Glu Ala Ser Leu Ala
35 40 45

Gln Leu Ile Ser Ala Leu Arg Gln His Arg Arg Asn Asp Val Val Glu
50 55 60

Lys Ile Arg
65

<210> 22
<211> 68
<212> PRT
<213> Homo sapiens

<400> 22
Gln Val Lys Gly Phe Val Arg Lys Asn Gly Val Asn Glu Ala Lys Ile
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Asp Glu Ile Lys Asn Asp Asn Val Gln Asp Thr Ala Glu Gln Lys Val
20 25 30

Gln Leu Leu Arg Asn Trp His Gln Leu His Gly Lys Lys Glu Ala Tyr
35 40 45

Asp Thr Leu Ile Lys Asp Leu Lys Lys Ala Asn Leu Cys Thr Leu Ala
50 55 60

Glu Lys Ile Gln
65

<210> 23
<211> 68
<212> PRT
<213> Homo sapiens

<400> 23
Arg Trp Lys Glu Phe Val Arg Arg Leu Gly Leu Ser Asp His Glu Ile
1 5 10 15

Asp Arg Leu Glu Leu Gln Asn Gly Arg Cys Leu Arg Glu Ala Gln Tyr
20 25 30

Ser Met Leu Ala Thr Trp Arg Arg Arg Thr Arg Arg Glu Ala Thr Leu
35 40 45

Glu Leu Leu Gly Arg Val Leu Arg Asp Met Asp Leu Leu Gly Cys Leu
50 55 60

Glu Asp Ile Glu
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<210> 24

<211> 65
<212> PRT
<213> Homo sapiens

<400> 24
Arg Trp Lys Glu Phe Val Arg Thr Leu Gly Leu Arg Glu Ala Glu Ile
1 5 10 15

Glu Ala Val Glu Val Glu Ile Gly Arg Phe Arg Asp Gln Gln Tyr Glu
20 25 30

Met Leu Lys Arg Trp Arg Gln Gln Gln Pro Ala Gly Leu Gly Ala Val
35 40 45

Tyr Ala Ala Leu Glu Arg Met Gly Leu Asp Gly Cys Val Glu Asp Leu
50 55 60

Arg
65

<210> 25
<211> 67
<212> PRT
<213> Homo sapiens

<400> 25
Ser Trp Asp Gln Leu Met Arg Gln Leu Asp Leu Thr Lys Asn Glu Ile
1 5 10 15

Asp Val Val Arg Ala Gly Thr Ala Gly Pro Gly Asp Ala Leu Tyr Ala
20 25 30

Met Leu Met Lys Trp Val Asn Lys Thr Gly Arg Asn Ala Ser Ile His
35 40 45

Thr Leu Leu Asp Ala Leu Glu Arg Met Glu Glu Arg His Ala Lys Glu
50 55 60

Lys Ile Gln
65

<210> 26
<211> 67
<212> PRT
<213> Homo sapiens

<400> 26
Ser Trp Glu Pro Leu Met Arg Lys Leu Gly Leu Met Asp Asn Glu Ile
1 5 10 15

Lys Val Ala Lys Ala Glu Ala Ala Gly His Arg Asp Thr Leu Tyr Thr
20 25 30

Met Leu Ile Lys Trp Val Asn Lys Thr Gly Arg Asp Ala Ser Val His
35 40 45

Thr Leu Leu Asp Ala Leu Glu Thr Leu Gly Glu Arg Leu Ala Lys Gln
50 55 60

Lys Ile Glu
65

<210> 27
<211> 733
<212> DNA
<213> Homo sapiens

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tctcccggac tcctgaggtc acatgcgtgg tggtggacgt aagccacgaa gaccctgagg 180
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ggctgaatgg caaggagtac aagtgcaagg tctccaacaa agccctccca acccccatcg 360
agaaaaccat ctccaaagcc aaagggcagc cccgagaacc acaggtgtac accctgcccc 420
catcccggga tgagctgacc aagaaccagg tcagcctgac ctgcctggtc aaaggcttct 480
atccaagcga catcgccgtg gagtgggaga gcaatgggca gccggagaac aactacaaga 540
ccacgcctcc cgtgctggac tccgacggct ccttcttcct ctacagcaag ctcaccgtgg 600
acaagagcag gtggcagcag gggaacgtct tctcatgctc cgtgatgcat gaggctctgc 660
acaaccacta cacgcagaag agcctctccc tgtctccggg taaatgagtg cgacggccgc 720
gactctagag gat 733